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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/935,757

DATE: 12/11/2001

TIME: 16:06:24

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3 <110> APPLICANT: MOCKEL, BETTINA
4   HERMANN, THOMAS
5   FARWICK, MIKE
6   BINDER, MICHAEL
7   PFEFFERLE, WALTER
9 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE SIGE GENE
11 <130> FILE REFERENCE: MAS/21123/282664
13 <140> CURRENT APPLICATION NUMBER: 09/935,757
14 <141> CURRENT FILING DATE: 2001-08-24
16 <150> PRIOR APPLICATION NUMBER: 60/295,009
17 <151> PRIOR FILING DATE: 2001-06-04
19 <150> PRIOR APPLICATION NUMBER: DE 100 43 336.7
20 <151> PRIOR FILING DATE: 2000-09-02
22 <150> PRIOR APPLICATION NUMBER: DE 101 26 422.4
23 <151> PRIOR FILING DATE: 2001-05-31
25 <160> NUMBER OF SEQ ID NOS: 8
27 <170> SOFTWARE: PatentIn Ver. 2.1
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31 <212> TYPE: DNA
32 <213> ORGANISM: Corynebacterium glutamicum
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (302)..(949)
37 <223> OTHER INFORMATION: sigE gene
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44 gtccggtttca gtagtggaact cgacataagt gcgaagatac tcgaaggcgt tactcacgcg 180
46 ttatagtcta gagcgcagcag gcgagatgtg aagtacctac acgcattaag tgcaaataaa 240
48 ttcacaattg ccagaagatg cacaggatgt aatctagatt tcccaagttc agtggggcaa 300
50 a atg act tat atg aaa aag aag tcc cga gat gac gca ccc gtc gta atc 349
51 Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile
52 1 5 10 15
54 gaa acc gtt caa gca gaa cat gct gaa gaa ctc acg ggc act gca gca 397
55 Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala
56 20 25 30
58 ttc gat gct gga cag gca gac atg cca aca tgg ggc gag cta gtc gca 445
59 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
60 35 40 45
62 gaa cat gca gat agc gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac 493
63 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
64 50 55 60
66 cag cac gat gct gaa gac ctg acc caa gaa aca ttc atg cgt gtc ttc 541
67 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
68 65 70 75 80
70 cgc tcg ttg aag agc tac cag cca ggc acc ttt gag ggc tgg ctg cac 589

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71 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
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75 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
76      100      105      110
78 atc cgc atg gag gcg ctg cct gaa gat tat gag cgc gtt ccg ggc aat 685
79 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
80      115      120      125
82 gac atc acc cca gag cag gca tac acc gaa gct aac ctt gac cca gct 733
83 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
84      130      135      140
86 ctg cag gca gcc ctc gat gag ttg agc cca gac ttc cgc gtg gca gtg 781
87 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
88 145      150      155      160
90 atc ctc tgt gat gtt gtt ggt atg agc tat gac gaa atc gca gag acc 829
91 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
92      165      170      175
94 ctc gga gtg aaa atg ggt acc gtg cgt tcc cgt att cac cgt gga cgc 877
95 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
96      180      185      190
98 agc cag ctt cgt gca agt ttg gaa gct gca gca atg acc agc gag gaa 925
99 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu
100      195      200      205
102 gtt tct ttg ttg gtt cca acc cac taaagttggt gtgtttttctg acacgacaaa 979
103 Val Ser Leu Leu Val Pro Thr His
104      210      215
106 cgcaaattgtc gtgtcatttt tgcagctcag tgcattatatt tgggggttcgt ggtgctggaca 1039
108 gggaaatttat cacaggcgac atccgttttt agtagtaggt atcttggata agaagttacc 1099
110 cacatccttg aaagtcgaga cacaggaggt catcggaaga tatgttcaat tccgacacca 1159
112 ccgcgaatct ccaagctaaa agtcgagatc gtgcaggatc taaagcaaag cgcagcaggc 1219
114 caagttttga ttcagtagcg cgggatgttt tggatgttcg aacaaaaaca gcacaagtta 1279
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126 1      5      10      15
128 Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala
129      20      25      30
131 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
132      35      40      45
134 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
135      50      55      60
137 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
138 65      70      75      80
140 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
141      85      90      95

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143 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
144           100           105           110
146 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
147           115           120           125
149 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
150           130           135           140
152 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
153 145           150           155           160
155 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
156           165           170           175
158 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
159           180           185           190
161 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu
162           195           200           205
164 Val Ser Leu Leu Val Pro Thr His
165           210           215
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169 <211> LENGTH: 457
170 <212> TYPE: DNA
171 <213> ORGANISM: Corynebacterium glutamicum
173 <220> FEATURE:
174 <223> OTHER INFORMATION: upstream region
176 <400> SEQUENCE: 3
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178 aacgaatata ttcacggtcg tcacgtgctg cttgggtgtc acgatccttg cgggtttgat 120
179 ccgcaatggg gccgtcaagg agcgcatcgg cgagcaccag cgcaccgcct cgtcgaagaa 180
180 gcggccaggc ggcgtcgaca agcgcttta aatccatggg ggagacttgg ccgaagacaa 240
181 gctgatagct gtcgttggca agcgactca tcacgtcgag cgggcgcgag agcaagaagc 300
182 gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgctgatgct 360
183 ctgattcagg atcaatgcag gtcagtgtgg tgttatcggc cagtccgttc aggatataca 420
184 gacccaccaa ccggcagcc ggggtaatcg cgatggc 457
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 299
189 <212> TYPE: DNA
190 <213> ORGANISM: Corynebacterium glutamicum
192 <220> FEATURE:
193 <223> OTHER INFORMATION: downstream region
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197 ttgtgcactg cgctgaatgt agggaagaga ttaaccgtca gcgggaaacc gttgattatc 120
198 tccgctcaga gtgcaaaac gaagaagtgt ccgcccacat ggacctcaaa gcacggcttg 180
199 ccagcctcgc cactgagtgc atgcctggcc ctggcgcgaga gaatttagca atgcagcgcc 240
200 cagagtcttt tgtggctaaa gttgagtccg tagtgcgcg agttcgtaag aaccaaggc 299
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204 <211> LENGTH: 2086
205 <212> TYPE: DNA
206 <213> ORGANISM: Corynebacterium glutamicum
208 <220> FEATURE:
209 <221> NAME/KEY: CDS

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211 <223> OTHER INFORMATION: sigE
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218 ccgcaatggg gccgtcaagg agcgcacatcg cgagcaccag cgcaccgcct cgtcgaagaa 180
220 gcggccaggc ggcgtcgaca agcgccttta aatccatggg ggagacttgg ccgaagacaa 240
222 gctgatatgt gtcgttggca aggcgactca tcacgtcgag cgggcgcgag agcaagaagc 300
224 gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgctgatgct 360
226 ctgattcagg atcaatgcag gtcagtgtgg tggtatcggc cagtccgttc aggatataca 420
228 gacccaccaaa cccggcagcc ggggtaatcg cgatggcacc agtggagccg ttgccattgg 480
230 tgggtggcagc caaagtgggt agcagctggc cagtcatttc atccggggcg gggagaccga 540
232 actcggcggc gtcttcacga gcgcgcgcta cagcagcgtc ggtttcagta gtggactcga 600
234 cataagtgcg aagatactcg aaggcgttac tcacgcgcta tagtctagag cgagcaggcg 660
236 agatgtgaag tacctacacg cattaagtgc aaatgaattc acaattgcca gaagatgcac 720
238 aggatgtaat ctagatttcc caagttcagt ggggcaaaa atg act tat atg aaa aag 776
239                                     Met Thr Tyr Met Lys Lys
240                                     1           5
242 aag tcc cga gat gac gca ccc gtc gta atc gaa acc gtt caa gca gaa 824
243 Lys Ser Arg Asp Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala Glu
244          10          15          20
246 cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag gca 872
247 His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln Ala
248          25          30          35
250 gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc gtt 920
251 Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser Val
252          40          45          50
254 tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa gac 968
255 Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu Asp
256          55          60          65          70
258 ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc tac 1016
259 Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser Tyr
260          75          80          85
262 cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac ttg 1064
263 Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn Leu
264          90          95          100
266 ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg ctg 1112
267 Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala Leu
268          105          110          115
270 cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag cag 1160
271 Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu Gln
272          120          125          130
274 gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc gat 1208
275 Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu Asp
276          135          140          145          150
278 gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt gtt 1256
279 Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val Val
280          155          160          165
282 ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg ggt 1304

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283 Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met Gly
284      170      175      180
286 acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca agt 1352
287 Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala Ser
288      185      190      195
290 ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt cca 1400
291 Leu Glu Ala Ala Ala Met Thr Ser Glu Glu Val Ser Leu Leu Val Pro
292      200      205      210
294 acc cac taaagttggt gtgttttctg acacgcacaaa cgcaaagtgc gtgtcatttt 1456
295 Thr His
296 215
298 tgcagctcag tgcattatatt tgggggttcgt ggtgcggaca gggaaacttat cacaggcgac 1516
300 atccgttttg agtagtaggt atcttggata agaagttacc cacatccttg aaagtcgaga 1576
302 cacaggaggt catcggaaga tatgttcaat tccgacacca ccgcgaatct ccaagctaaa 1636
304 agtcgagatc gtgcaggatc taaagcaaaag cgcagcaggc caagttttga ttcagtagcg 1696
306 cgggatgttt tggatgttcg aacaaaaaca gcacaagtta aaaacaaggc taaagagttt 1756
308 tcctctgttg atcacctttc agcagacgcc gcagccatgt ttgtagacaa tgaactgtcc 1816
310 cgtggcgcca tgcacgcgc caggctgcac attgtgcact gcgctgaatg tagggaagag 1876
312 attaaccgtc agcgggaaac cgttgattat ctccgctcag agtgcaaaaa cgaagaagtg 1936
314 tccgcccāaa tggacctcaa agcacggctt gccagcctcg ccactgagtg catgcctggc 1996
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331 20 25 30
333 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
334 35 40 45
336 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
337 50 55 60
339 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
340 65 70 75 80
342 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
343 85 90 95
345 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
346 100 105 110
348 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
349 115 120 125
351 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
352 130 135 140
354 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
355 145 150 155 160
357 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
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VERIFICATION SUMMARY

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